GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 8, 2006, 14:25:10 ; Search time 1573 Seconds
                                      (without alignments)
                                      10824.596 Million cell updates/sec

Title: US-10-612-594-1
Perfect score: 9100
Sequence: a accggtggcgaggacaaca..........cagtgcctcaaaggttgga 9100

Scoring table: IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Database :   Issued_Patents_NA:*
        1:    /EMC_Celerra_SIDS3/ptodata#2/ina/1_COMB.seq:*
        2:    /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
        3:    /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
        4:    /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
        5:    /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
        6:    /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
        7:    /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
        8:    /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
        9:    /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
       10:    /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	138.4	1.5	5511	3	US-08-928-361B-2	Sequence 2, Appli
c 2	138.4	1.5	5511	3	US-09-588-995A-2	Sequence 2, Appli
c 3	138.4	1.5	7334	3	US-08-928-361B-1	Sequence 1, Appli
c 4	138.4	1.5	7334	3	US-09-588-995A-1	Sequence 1, Appli
c 5	125	1.4	5163	3	US-08-700-651-1	Sequence 1, Appli
c 6	125	1.4	5163	3	US-08-928-361B-4	Sequence 4, Appli
c 7	125	1.4	5163	3	US-09-588-995A-4	Sequence 4, Appli
c 8	125	1.4	5318	3	US-08-700-651-2	Sequence 2, Appli
c 9	125	1.4	5318	3	US-08-928-361B-3	Sequence 3, Appli
c 10	125	1.4	5318	3	US-09-588-995A-3	Sequence 3, Appli
c 11	113.8	1.3	3486	3	US-09-614-221A-292	Sequence 292, App
c 12	110.8	1.2	867	3	US-09-216-393B-340	Sequence 340, App
c 13	110.8	1.2	867	3	US-09-216-393B-342	Sequence 342, App
c 14	110.8	1.2	1397	3	US-09-216-393B-343	Sequence 343, App
c 15	110.8	1.2	1397	3	US-09-216-393B-345	Sequence 345, App
c 16	103.2	1.1	601	3	US-09-949-016-180704	Sequence 180704,
c 17	103.2	1.1	70770	3	US-09-949-016-16938	Sequence 16938, A
c 18	98	1.1	83428	3	US-09-949-016-13610	Sequence 13610, A
c 19	95.6	1.1	8045	5	US-09-913-878A-1	Sequence 1, Appli
c 20	90.6	1.0	19124	2	US-08-487-826B-13	Sequence 13, Appli
c 21	82.8	0.9	8442	3	US-09-272-032-6	Sequence 6, Appli
c 22	80.2	0.9	7218	2	US-08-232-463-14	Sequence 14, Appl
c 23	79.8	0.9	1037	3	US-09-181-585-3	Sequence 3, Appli
c 24	79.8	0.9	1159	3	US-09-181-585-1	Sequence 1, Appli
c 25	79.4	0.9	1471	3	US-09-181-585-2	Sequence 2, Appli
c 26	79.4	0.9	43795	3	US-08-742-185-101	Sequence 101, App
c 27	78.6	0.9	1671	3	US-09-248-796A-8235	Sequence 8235, Ap
c 28	78	0.9	2032	3	US-09-241-581B-5	Sequence 5, Appli
c 29	78	0.9	2032	3	US-08-265-428-5	Sequence 5, Appli
c 30	78	0.9	2032	7	PCT-US95-07721-5	Sequence 5, Appli
c 31	77	0.8	1149	3	US-09-248-796A-9133	Sequence 9133, Ap
c 32	76.6	0.8	147382	3	US-09-949-016-14624	Sequence 14624, A
c 33	76.4	0.8	3001	3	US-09-539-333D-215	Sequence 215, App
c 34	75.2	0.8	3337	3	US-08-072-610-1	Sequence 1, Appli
c 35	75.2	0.8	3337	2	US-08-719-822B-1	Sequence 1, Appli
c 36	75.2	0.8	3337	3	US-09-092-458-1	Sequence 1, Appli
c 37	75.2	0.8	3337	3	US-08-719-821C-1	Sequence 1, Appli
c 38	74.8	0.8	740	3	US-09-451-117-1	Sequence 1, Appli
c 39	74.8	0.8	740	3	US-09-888-655-1	Sequence 1, Appli
c 40	74.8	0.8	740	3	US-09-888-501-1	Sequence 1, Appli
c 41	74.6	0.8	1485	3	US-09-248-796A-2443	Sequence 2443, Ap
c 42	74.2	0.8	1671	3	US-09-614-221A-554	Sequence 554, App
c 43	74.2	0.8	1671	3	US-09-487-558B-425	Sequence 425, App
c 44	74	0.8	52202	3	US-09-949-016-17006	Sequence 17006, A
c 45	73.8	0.8	198	7	PCT-US95-10668-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-928-361B-2/c
; Sequence 2, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
; APPLICANT: Petersen, Carolyn
; TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
; TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
; TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: SPECIES INFECTIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PETERS, VERNY, JONES & BIKSA
;   STREET: 385 Sherman Avenue, Suite 6
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94306-1840
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08,928,361B
;   FILING DATE: 12-SEP-1997
;   CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/026,062
;   FILING DATE: 13-SEP-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Verny, Hana
;   REGISTRATION NUMBER: 30,518
;   REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650-324-1677
;   TELEFAX: 650-324-1678
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 5511 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-08-928-361B-2